

RAW SEQUENCE LISTING

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Application Serial Number: 10/568,033
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PATENT APPLICATION: US/10/568,033

DATE: 11/15/2006
TIME: 11:50:15

Input Set : A:\SPO-125.ST25.txt
Output Set: N:\CRF4\11152006\J568033.raw

3 <110> APPLICANT: Nakajima, Toshihiro
4 Amano, Tetsuya
5 Yagashita, Naoko
7 <120> TITLE OF INVENTION: THERAPEUTIC PREPARATION FOR HEMATOPOIETIC DISEASE
9 <130> FILE REFERENCE: BHP-A0301P
11 <140> CURRENT APPLICATION NUMBER: US 10/568,033
12 <141> CURRENT FILING DATE: 2006-02-10
14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/011951
15 <151> PRIOR FILING DATE: 2004-08-13
17 <150> PRIOR APPLICATION NUMBER: US 60/495,001
18 <151> PRIOR FILING DATE: 2003-08-13
20 <160> NUMBER OF SEQ ID NOS: 4
22 <170> SOFTWARE: PatentIn Ver. 2.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 3374
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (403)..(2256)
33 <400> SEQUENCE: 1
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36 ttgattgttag atatagggtct ctccttgca aggttaattag gtccttaaa ttacctgtaa 120
38 gattttcttg ccacagcatc cattctgggtt aggctggta tcttcgtgagt agtgatagat 180
40 tgggtggtgg tgagggttac aggtgttccc ttctcttact cctgggtgttgc gctacaatca 240
42 gttggcgtct agagcagcat gggacagggtt ggttaaggggaa gtcttctcat tatgcagaag 300
44 tgcataactt aaatctctgt cagatctacc tttatgttagc cccgcagtcg cgcggattga 360
46 gcgggctcgc ggcgctgggt tcctggtctc cgggcagggg ca atg ttc cgc acg 414
47 Met Phe Arg Thr
48 1
50 gca gtg atg atg gcg gcc agc ctg gcg ctg acc ggg gct gtg gtg gct 462
51 Ala Val Met Met Ala Ala Ser Leu Ala Leu Thr Gly Ala Val Val Ala
52 5 10 15 20
54 cac gcc tac tac ctc aaa cac cag ttc tac ccc act gtg gtg tac ctg 510
55 His Ala Tyr Tyr Leu Lys His Gln Phe Tyr Pro Thr Val Val Tyr Leu
56 25 30 35
58 acc aag tcc agc ccc agc atg gca gtc ctg tac atc cag gcc ttt gtc 558
59 Thr Lys Ser Ser Pro Ser Met Ala Val Leu Tyr Ile Gln Ala Phe Val
60 40 45 50
62 ctt gtc ttc ctt ctg ggc aag gtg atg ggc aag gtg ttc ttt ggg caa 606
63 Leu Val Phe Leu Leu Gly Lys Val Met Gly Lys Val Phe Phe Gly Gln
64 55 60 65
66 ctg agg gca gca gag atg gag cac ctt ctg gaa cgt tcc tgg tac gcc 654

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67	Leu	Arg	Ala	Ala	Glu	Met	Glu	His	Leu	Leu	Glu	Arg	Ser	Trp	Tyr	Ala	
68	70				75						80						
70	gtc	aca	gag	act	tgt	ctg	gcc	ttc	acc	gtt	ttt	cgg	gat	gac	ttc	agc	702
71	Val	Thr	Glu	Thr	Cys	Leu	Ala	Phe	Thr	Val	Phe	Arg	Asp	Asp	Phe	Ser	
72	85				90						95					100	
74	ccc	cgc	ttt	gtt	gca	ctc	ttc	act	ctt	ctt	ctc	ttc	ctc	aaa	tgt	ttc	750
75	Pro	Arg	Phe	Val	Ala	Leu	Phe	Thr	Leu	Leu	Phe	Leu	Lys	Cys	Phe		
76					105					110					115		
78	cac	tgg	ctg	gct	gag	gac	cgt	gtg	gac	ttt	atg	gaa	cgc	agc	ccc	aac	798
79	His	Trp	Leu	Ala	Glu	Asp	Arg	Val	Asp	Phe	Met	Glu	Arg	Ser	Pro	Asn	
80					120					125			130				
82	atc	tcc	tgg	ctc	ttt	cac	tgc	cgc	att	gtc	tct	ctt	atg	ttc	ctc	ctg	846
83	Ile	Ser	Trp	Leu	Phe	His	Cys	Arg	Ile	Val	Ser	Leu	Met	Phe	Leu	Leu	
84					135					140			145				
86	ggc	atc	ctg	gac	ttc	ctc	ttc	gtc	agc	cac	gcc	tat	cac	agc	atc	ctg	894
87	Gly	Ile	Leu	Asp	Phe	Leu	Phe	Val	Ser	His	Ala	Tyr	His	Ser	Ile	Leu	
88					150					155			160				
90	acc	cgt	ggg	gcc	tct	gtg	cag	ctg	gtg	ttt	ggc	tat	gag	tat	gcc	atc	942
91	Thr	Arg	Gly	Ala	Ser	Val	Gln	Leu	Val	Phe	Gly	Phe	Glu	Tyr	His	Ile	
92	165				170					175			180				
94	ctg	atg	acg	atg	gtg	ctc	acc	atc	ttc	atc	aag	tat	gtg	ctg	cac	tcc	990
95	Leu	Met	Thr	Met	Val	Leu	Thr	Ile	Phe	Ile	Lys	Tyr	Val	Leu	His	Ser	
96					185					190			195				
98	gtg	gac	ctc	cag	agt	gag	aac	ccc	tgg	gac	aac	aag	gct	gtg	tac	atg	1038
99	Val	Asp	Leu	Gln	Ser	Glu	Asn	Pro	Trp	Asp	Asn	Lys	Ala	Val	Tyr	Met	
100					200					205			210				
102	ctc	tac	aca	gag	ctg	ttt	aca	ggc	ttc	atc	aag	gtt	ctg	ctg	tac	atg	1086
103	Leu	Tyr	Thr	Glu	Leu	Phe	Thr	Gly	Phe	Ile	Lys	Val	Leu	Tyr	Met		
104					215					220			225				
106	gcc	ttc	atg	acc	atc	atg	atc	aag	gtg	cac	acc	ttc	cca	ctc	ttt	gcc	1134
107	Ala	Phe	Met	Thr	Ile	Met	Ile	Lys	Val	His	Thr	Phe	Pro	Leu	Phe	Ala	
108					230					235			240				
110	atc	cgg	ccc	atg	tac	ctg	gcc	atg	aga	cag	ttc	aag	aaa	gct	gtg	aca	1182
111	Ile	Arg	Pro	Met	Tyr	Leu	Ala	Met	Arg	Gln	Phe	Lys	Lys	Ala	Val	Thr	
112	245				250					255			260				
114	gat	gcc	atc	atg	tct	cgc	cga	gcc	atc	cgc	aac	atg	aac	acc	ctg	tat	1230
115	Asp	Ala	Ile	Met	Ser	Arg	Arg	Ala	Ile	Arg	Asn	Met	Asn	Thr	Leu	Tyr	
116					265					270			275				
118	cca	gat	gcc	acc	cca	gag	gag	ctc	cag	gca	atg	gac	aat	gtc	tgc	atc	1278
119	Pro	Asp	Ala	Thr	Pro	Glu	Glu	Leu	Gln	Ala	Met	Asp	Asn	Val	Cys	Ile	
120					280					285			290				
122	atc	tgc	cga	gaa	gag	atg	gtg	act	ggt	gcc	aag	aga	ctg	ccc	tgc	aac	1326
123	Ile	Cys	Arg	Glu	Glu	Met	Val	Thr	Gly	Ala	Lys	Arg	Leu	Pro	Cys	Asn	
124					295					300			305				
126	cac	att	ttc	cat	acc	agc	tgc	ctg	cgc	tcc	tgg	ttc	cag	cgg	cag	cag	1374
127	His	Ile	Phe	His	Thr	Ser	Cys	Leu	Arg	Ser	Trp	Phe	Gln	Arg	Gln	Gln	
128					310					315			320				
130	acc	tgc	ccc	acc	tgc	cgt	atg	gat	gtc	ctt	cgt	gca	tcg	ctg	cca	gcg	1422
131	Thr	Cys	Pro	Thr	Cys	Arg	Met	Asp	Val	Leu	Arg	Ala	Ser	Leu	Pro	Ala	

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132	325	330	335	340	
134	cag tca cca cca ccc ccg gag cct gcg gat	cag ggg cca ccc cct gcc		1470	
135	Gln Ser Pro Pro Pro Pro Glu Pro Ala Asp	Gln Gly Pro Pro Pro Ala			
136	345	350	355		
138	ccc cac ccc cca cca ctc ttg cct cag	ccc ccc aac ttc ccc cag ggc		1518	
139	Pro His Pro Pro Pro Leu Leu Pro Gln	Pro Pro Asn Phe Pro Gln Gly			
140	360	365	370		
142	ctc ctg cct cct ttt cct cca ggc atg ttc	cca ctg tgg ccc ccc atg		1566	
143	Leu Leu Pro Pro Phe Pro Pro Gly Met	Phe Pro Leu Trp Pro Pro Met			
144	375	380	385		
146	ggc ccc ttt cca cct gtc ccg cct	ccc ccc agc tca gga gag gct gtg		1614	
147	Gly Pro Phe Pro Pro Val Pro Pro Pro Ser	Ser Gly Glu Ala Val			
148	390	395	400		
150	gct cct cca tcc acc agt gca gca gcc	ttt tct cgg ccc agt gga gca		1662	
151	Ala Pro Pro Ser Thr Ser Ala Ala Leu	Ser Arg Pro Ser Gly Ala			
152	405	410	415	420	
154	gct aca acc aca gct gtc acc agt	gct act gct gct tct gcc aca		1710	
155	Ala Thr Thr Thr Ala Ala Gly Thr Ser	Ala Thr Ala Ala Ser Ala Thr			
156	425	430	435		
158	gca tct ggc cca ggc tct ggc tct	gcc cca gag gct ggc cct gcc cct		1758	
159	Ala Ser Gly Pro Gly Ser Gly Ser Ala	Pro Glu Ala Gly Pro Ala Pro			
160	440	445	450		
162	ggt ttc ccc ttc cct ccc tgg atg ggt	atg ccc ctg cct cca ccc		1806	
163	Gly Phe Pro Phe Pro Pro Trp Met Gly	Met Pro Leu Pro Pro Pro			
164	455	460	465		
166	ttt gcc ttc ccc cca atg cct gtg	ccc cct gcg ggc ttt gct ggg ctg		1854	
167	Phe Ala Phe Pro Pro Met Pro Val Pro	Pro Ala Gly Phe Ala Gly Leu			
168	470	475	480		
170	acc cca gag gag cta cga gct ctg	gag ggc cat gag cgg cag cac ctg		1902	
171	Thr Pro Glu Glu Leu Arg Ala Leu Glu	Gly His Glu Arg Gln His Leu			
172	485	490	495	500	
174	gag gcc cgg ctg cag agc ctg cgt	aac atc cac aca ctg ctg gac gcc		1950	
175	Glu Ala Arg Leu Gln Ser Leu Arg Asn	Ile His Thr Leu Leu Asp Ala			
176	505	510	515		
178	gcc atg ctg cag atc aac cag tac	ctc acc gtg ctg gcc tcc ttg ggg		1998	
179	Ala Met Leu Gln Ile Asn Gln Tyr	Leu Thr Val Leu Ala Ser Leu Gly			
180	520	525	530		
182	ccc ccc cgg cct gcc act tca gtc	aac tcc act gag ggg act gcc act		2046	
183	Pro Pro Arg Pro Ala Thr Ser Val	Asn Ser Thr Glu Gly Thr Ala Thr			
184	535	540	545		
186	aca gtt gtt gct gct gcc tcc	tcc acc agc atc cct agc tca gag gcc		2094	
187	Thr Val Val Ala Ala Ser Ser Thr	Ser Ile Pro Ser Ser Glu Ala			
188	550	555	560		
190	acg acc cca acc cca gga gcc tcc	cca cca gcc cct gaa atg gaa agg		2142	
191	Thr Thr Pro Thr Pro Gly Ala Ser	Pro Pro Ala Pro Glu Met Glu Arg			
192	565	570	575	580	
194	cct cca gct cct gag tca gtg	ggc aca gag gag atg cct gag gat gga		2190	
195	Pro Pro Ala Pro Glu Ser Val Gly	Thr Glu Glu Met Pro Glu Asp Gly			
196	585	590	595		

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198 gag ccc gat gca gca gag ctc cgc cgg cgc ctg cag aag ctg gag 2238
199 Glu Pro Asp Ala Ala Glu Leu Arg Arg Arg Arg Leu Gln Lys Leu Glu
200 600 605 610
202 tct cct gtt gcc cac tga cactgccccca gcccagcccc agcctctgct 2286
203 Ser Pro Val Ala His
204 615
206 ctttgagca gcccctcgctg gaacatgtcc tgccaccaag tgccagctcc ctctctgtct 2346
208 gcaccaggga gtagtacccc cagctctgag aaagaggcgg catccccatg gccaagtgg 2406
210 aagaggctgg gggttccatt tgactccagt cccagggcgc catggggatc tcgggtcagt 2466
212 tccaggcctt ctctccaact cttcagccct gtgttctgct gggggcatga aggccagaagg 2526
214 tttagcctct gagaagccct cttcttcccc caccctttc caggagaagg ggctgcccct 2586
216 ccaagcccta cttgtatgtg cggagtacca ctgcagtgcc gaacagtatt agctccgtt 2646
218 cccaagtgtg gactccagag gggctggagg caagctatga acttgctcgc tggcccaccc 2706
220 ctaagactgg tacccatttc ctttcttac cctgatctcc ccagaaggct cttgtgtgg 2766
222 tgctgtgcc ccctatgccc tttggcatt ctgcgtctt ctggcaacca cacaactcag 2826
224 gaaaaggaaat gcctggagt ggggggtgcag gcgggcagca ctgagggacc ctgccccgccc 2886
226 cctcccccca gggcccttcc ccctgcagct tctcaagtga gactgacctg tctcacccag 2946
228 cagccactgc ccagccgcac tccaggcaag ggccagtgcg cctgctccctg accactgcaa 3006
230 tcccagcgcc caaggaaggc cacttctcaa ctggcagaac ttctgaagtt tagaattgg 3066
232 attacttcct tactagtgtc tttggctt aattttgtct tttgaagttt aatgcttaat 3126
234 cccgggaaag aggaacagga gtgccagact cctggcttt ccagttttaga aaaggctctg 3186
236 tgccaaggag ggaccacagg agctgggacc tgccctcccc tgcctttcc ccttgggttt 3246
238 gtgttacaag agttgttggaa gacagttca gatgattatt taatttgtaa atattgtaca 3306
240 aatttaataa gcttaaattt tatatacagc caaataaaaaa cttgcattaa caaaaaaaaaa 3366
242 aaaaaaaaaa 3374
245 <210> SEQ ID NO: 2
246 <211> LENGTH: 617
247 <212> TYPE: PRT
248 <213> ORGANISM: Homo sapiens
250 <400> SEQUENCE: 2
251 Met Phe Arg Thr Ala Val Met Met Ala Ala Ser Leu Ala Leu Thr Gly
252 1 5 10 15
254 Ala Val Val Ala His Ala Tyr Tyr Leu Lys His Gln Phe Tyr Pro Thr
255 20 25 30
257 Val Val Tyr Leu Thr Lys Ser Ser Pro Ser Met Ala Val Leu Tyr Ile
258 35 40 45
260 Gln Ala Phe Val Leu Val Phe Leu Leu Gly Lys Val Met Gly Lys Val
261 50 55 60
263 Phe Phe Gly Gln Leu Arg Ala Ala Glu Met Glu His Leu Leu Glu Arg
264 65 70 75 80
266 Ser Trp Tyr Ala Val Thr Glu Thr Cys Leu Ala Phe Thr Val Phe Arg
267 85 90 95
269 Asp Asp Phe Ser Pro Arg Phe Val Ala Leu Phe Thr Leu Leu Phe
270 100 ~105 110
272 Leu Lys Cys Phe His Trp Leu Ala Glu Asp Arg Val Asp Phe Met Glu
273 115 120 125
275 Arg Ser Pro Asn Ile Ser Trp Leu Phe His Cys Arg Ile Val Ser Leu
276 130 135 140
278 Met Phe Leu Leu Gly Ile Leu Asp Phe Leu Phe Val Ser His Ala Tyr

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279	145	150	155	160
281	His Ser Ile Leu Thr Arg Gly Ala Ser Val Gln Leu Val Phe Gly Phe			
282		165	170	175
284	Glu Tyr Ala Ile Leu Met Thr Met Val Leu Thr Ile Phe Ile Lys Tyr			
285		180	185	190
287	Val Leu His Ser Val Asp Leu Gln Ser Glu Asn Pro Trp Asp Asn Lys			
288		195	200	205
290	Ala Val Tyr Met Leu Tyr Thr Glu Leu Phe Thr Gly Phe Ile Lys Val			
291		210	215	220
293	Leu Leu Tyr Met Ala Phe Met Thr Ile Met Ile Lys Val His Thr Phe			
294		225	230	235
296	Pro Leu Phe Ala Ile Arg Pro Met Tyr Leu Ala Met Arg Gln Phe Lys			
297		245	250	255
299	Lys Ala Val Thr Asp Ala Ile Met Ser Arg Arg Ala Ile Arg Asn Met			
300		260	265	270
302	Asn Thr Leu Tyr Pro Asp Ala Thr Pro Glu Glu Leu Gln Ala Met Asp			
303		275	280	285
305	Asn Val Cys Ile Ile Cys Arg Glu Glu Met Val Thr Gly Ala Lys Arg			
306		290	295	300
308	Leu Pro Cys Asn His Ile Phe His Thr Ser Cys Leu Arg Ser Trp Phe			
309		305	310	315
311	Gln Arg Gln Gln Thr Cys Pro Thr Cys Arg Met Asp Val Leu Arg Ala			
312		325	330	335
314	Ser Leu Pro Ala Gln Ser Pro Pro Pro Glu Pro Ala Asp Gln Gly			
315		340	345	350
317	Pro Pro Pro Ala Pro His Pro Pro Pro Leu Leu Pro Gln Pro Pro Asn			
318		355	360	365
320	Phe Pro Gln Gly Leu Leu Pro Pro Phe Pro Pro Gly Met Phe Pro Leu			
321		370	375	380
323	Trp Pro Pro Met Gly Pro Phe Pro Pro Val Pro Pro Pro Pro Ser Ser			
324		385	390	395
326	Gly Glu Ala Val Ala Pro Pro Ser Thr Ser Ala Ala Ala Leu Ser Arg			
327		405	410	415
329	Pro Ser Gly Ala Ala Thr Thr Ala Ala Gly Thr Ser Ala Thr Ala			
330		420	425	430
332	Ala Ser Ala Thr Ala Ser Gly Pro Gly Ser Gly Ser Ala Pro Glu Ala			
333		435	440	445
335	Gly Pro Ala Pro Gly Phe Pro Phe Pro Pro Pro Trp Met Gly Met Pro			
336		450	455	460
338	Leu Pro Pro Pro Phe Ala Phe Pro Pro Met Pro Val Pro Pro Ala Gly			
339		465	470	475
341	Phe Ala Gly Leu Thr Pro Glu Glu Leu Arg Ala Leu Glu Gly His Glu			
342		485	490	495
344	Arg Gln His Leu Glu Ala Arg Leu Gln Ser Leu Arg Asn Ile His Thr			
345		500	505	510
347	Leu Leu Asp Ala Ala Met Leu Gln Ile Asn Gln Tyr Leu Thr Val Leu			
348		515	520	525
350	Ala Ser Leu Gly Pro Pro Arg Pro Ala Thr Ser Val Asn Ser Thr Glu			
351		530	535	540

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